

GenCore version 5.1.4 p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 01:10:18 ; Search time 18009 Seconds
(without alignments)
5843.509 Million cell updates/sec

Title: US-09-924-946-1

Perfect score: 3616

Sequence: 1 gattatgttggtgggtcggc.....gttgctcattgatgactgct 3616

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
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- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
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- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
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- 32: em_hg_other.*
- 33: em_hg_mus.*
- 34: em_hg_pln.*
- 35: em_hg_rod.*
- 36: em_hg_mam.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3616	100.0	3616	6	AX460870	AX460870 Sequence
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3	2844.4	78.7	2976	6	AX323479	AX323479 Sequence
4	2665.6	73.7	2736	6	AV036093	AV036093 Homo sapi
5	2597.2	71.8	2603	6	AX377787	AX377787 Sequence
6	2443.6	67.6	3608	4	AF529202	AF529202 Bos tauru
7	2269.4	62.8	2271	9	AF338441	AF338441 Homo sapi
8	2265.4	62.6	2322	9	BC007522	BC007522 Homo sapi
9	2263.2	62.6	2268	6	AX323481	AX323481 Sequence
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12	1730	47.8	2274	10	AF338440	AF338440 Mus muscu
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14	1235.8	34.2	182222	2	AC123374	AC123374 Rattus no
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17	767.4	21.2	2811	9	AF284815	AF284815 Homo sapi
18	765.8	21.2	2262	6	AR116983	AR116983 Sequence
19	765.8	21.2	2574	9	AF282619	AF282619 Homo sapi
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21	765.8	21.2	2920	6	AR116982	AR116982 Sequence
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23	738.4	20.4	3346	5	AF103901	AF103901 Perca fla
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39	199.2	5.5	2476	6	AR142625	AR142625 Sequence
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ALIGNMENTS

RESULT 1	AX460870	3616 bp	DNA	linear	PAT 08-JUL-2002
AX460870	Sequence 1 from Patent WO0212470.				
LOCUS	AX460870	3616 bp	DNA	linear	PAT 08-JUL-2002
DEFINITION	Sequence 1 from Patent WO0212470.				
ACCESSION	AX460870				
VERSION	AX460870.1	GI:21726122			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Evans,M.J., Scicchitano,M.S., Bapat,A.R., Beer,E., Bhat,R.A.,				
	Ferris,E., Mastromeni,R., Zhang,J. and Karathanasis,S.K.				
TITLE	A member of the lysyl oxidase gene family				

JOURNAL Patent: WO 0212470-A 1 14-FEB-2002;
Wyeth (US)
FEATURES Location/Qualifiers
1..3616
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 813 a 997 c 1065 g 741 t
ORIGIN

Query Match 100.0%; Score 3616; DB 6; Length 3616;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1141 ACCTCATCTCTGCCAGTGTCTGTGTCTCAGCTGGGCTTGGCTCTGCTGGGAGGCC 1200
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VERSION BC013153.1 GI:15341930
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3665)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalon@bcm.tmc.edu
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 13 Row: 1 Column: 10
This clone was selected for full length sequencing because it
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prediction.

FEATURES
source

Location/Qualifiers
1. 3665

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BASE COUNT	824 a	1021 c	1085 g	735 t
ORIGIN				

Query Match	97.6%	Score 3529.8	DB 9	Length 3665
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RESULT 3

AX323479

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sequence 1 from Patent WO0192495.

AX323479

AX323479.1

GI:18094234

2976 bp

DNA

linear

PAT 07-JAN-2002

REFERENCE

1 Meyers.R.
 AUTHORS A human lysyl oxidase (47765) and uses thereof
 TITLE Patent: WO 019495-A 1 06-DEC-2001;
 JOURNAL Millennium Pharmaceuticals, Inc. (US)

FEATURES

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AY036093

LOCUS

DEFINITION Homo sapiens lysyl oxidase-like 4 mRNA, complete cds.

ACCESSION AY036093

VERSION AY036093.1 GI:17861371

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Maki,J.M., Tikkanen,H. and Kivirikko,K.I.

TITLE Cloning and characterization of a fifth human lysyl oxidase isoenzyme: the third member of the lysyl oxidase-related subfamily with four scavenger receptor cysteine-rich domains

JOURNAL Matrix Biol. 20 (7), 493-496 (2001)

MEDLINE 21550107

PUBMED 11691589

REFERENCE

AUTHORS Maki,J.M., Tikkanen,H. and Kivirikko,K.I.

TITLE Direct Submission

JOURNAL Submitted (18-MAY-2001) Department of Medical Biochemistry, University of Oulu, P.O. Box 5000, Oulu 90014, Finland

FEATURES

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QY	612	CTTGGCAGTGCACAGACGATAGCCCAAGTCACTGAGGGAGCCCTGGAGGTGAAGTATGAG	671
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QY	1932	TGGGTTTTGGCACCAAGTGCACAGGCATTACACAGCATTTGAGGTCTTCACCCACTACGAC	1991
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QY	1992	CTCTCTACTCTCAATGGCTCCAAAGTGGCTGAGGGGCAAAAGGCGAGTTCTGTCTCGAG	2051
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Db	2183	ATCACAGATGTGGGCCCCGGGAAATTATCTTCCAGGTGATTTGTGAACCCCACTATGAA	2242	Db	3229	GGACTGGGCTTAAATGTGAGTCCC--CGAGTTTCTGGAC TGAACCTTTCCATTGAAATAA	3286
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QY	2352	CTGGACAGGAAACAGCTCTCAGGAACACCTCATCTGAAGCTGTCACTGCCACACTCTTA	2411	QY	3420	TTAGTTAAGGATGGAACTCTGGGAAAGGCCACCATTCCTGTGATGGGGCTCTGATTTGC	3479
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QY	2412	CTGTGCTGCCATACACAGATACCTCAGCTTATTGGAGCATGCTTTACAGAGTCCCA	2471	QY	3480	TCTTGTCTCAAGTGAATAAAACCCCATGCTGCTTCTT -GACATGATTTCTGATCTTTTCTC	3538
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LOCUS

AE338441

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PRI 11-JUL-2001

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Db	2161	TATGATGGGACACCGGCTCTGGCTGCACAACTGCCACACAGGAAATTCATACCCAGGCAAT	2220
Qy	2340	GCAGAACTCTCCCTGGAGGAGGACAGCGTCTCAGGAACAACCTCATCTGA	2390
Db	2221	GCAGAACTCTCCCTGGAGGAGGACAGCGTCTCAGGAACAACCTCATCTGA	2271
RESULT 8			
LOCUS	BC007522	2322 bp	mRNA linear PRI 12-JUL-2001
DEFINITION	Homo sapiens, clone MGC:14925 IMAGE:3353864, mRNA, complete cds.		
ACCESSION	BC007522		
VERSION	BC007522.1 GI:14043078		
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2322) Strausberg,R. Direct Submission Submitted (10-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA.		
REFERENCE	NIH-MGC Project URL: http://mgc.nci.nih.gov		
AUTHORS	Contact: MGC help desk		
JOURNAL	Email: cgapsb@mail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Genome Sequence Centre,		
	BC Cancer Agency, Vancouver, BC, Canada		
	info@bcsc.bc.ca		
REMARK	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,		
COMMENT	Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,		
	Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo		
	Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven		
	Ness, Pawan Pandoh, Anna-Liisa Prabhur, Parvaneh Saeedi, Jacqueline		
	Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,		
	Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,		
	George Yang, Scott Zuyderduyn, Marco Marra.		
	Clone distribution: MGC clone distribution information can be found		
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Series: IRAL Plate: 22 Row: p Column: 18		
	This clone was selected for full length sequencing because it		
	passed the following selection criteria: matched mRNA gi: 10438090.		

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ORIGIN			
Query Match		62.6%; Score 2265.4; IB 9; Length 2322;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 2266; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
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QY	1313	TGCTTGCCCAACATGAGAATGCTGCTGCTGTCTGAGTGCAAA1GTCCCTAAACATGGGCTTTCA	1372
Db	61	TGTTTGCACACATGAGAATGCTGCTGCTGTCTGAGTGCAAA1GTCCCTAAACATGGGCTTTCA	120
QY	1373	GAATCAGGTGCGCTTGGCTGGTGGCGGTATCCTCGAGCA(GGGCTATTGGAGTGTCAGGT	1432
Db	121	GAATCAGGTGCGCTTGGCTGGTGGCGGTATCCTCGAGCA(GGGCTATTGGAGTGTCAGGT	180
QY	1433	GGAGTGAACACGGGGTCCCAACCGCTGGGGGAGGCTGTGTGCAAG1GAAAACTGGGGCTCACCGA	1492
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QY	1493	AGCCATGGTGGCTGCGGACAGCTCGGCGCTGGTGTTCG(ATCCATGCTCAACAAGGAAC	1552
Db	241	AGCCATGGTGGCTGCGGACAGCTCGGCGCTGGTGTTCG(ATCCATGCTCAACAAGGAAC	300
QY	1553	CTGGTTCTGCTGGGGACCCCAAGGGCCACAGAGTGGTGTATGAGTGGGGTGGCTGTCTC	1612
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QY	1613	AGGCACAGAGTGGCGCTTCAGCAGCTGCAGAGCACCG(CGGTGCAGCTGCTCCACGG	1672
Db	361	AGGCACAGAGTGGCGCTTCAGCAGCTGCAGAGCACCG(CGGTGCAGCTGCTCCACGG	420
QY	1673	TGGCGGGCGCTTCTCCCTGGGTGGAGTCTCTGATGACAG1GCACCAGACCTGGTGATGAA	1732
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QY	1733	CGCCAGCTAGTGACAGGACAGCGGCTACTTGGAGACCG(CGGCTCAGCGAGCTGATTG	1792
Db	481	CGCCAGCTAGTGACAGGACAGCGGCTACTTGGAGACCG(CGGCTCAGCGAGCTGATTG	540
QY	1793	TGCCACAGGAGAACTGCCCTCTCCAAAGTCTCGCGATCA(ATGCACTGGCGCTACGATA	1852
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QY	1853	CGCGCGCTATTGGCGCTTCTCCACAGATCTACATCT(GGCCGAGCTGACTTTCGTC	1912
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QY	1913	AAAGACTGACCGCATAGTGGTGGTGGCCACAGTGCCA(AGGCATTACACAGCATTTGA	1972
Db	661	AAAGACTGACCGCATAGTGGTGGTGGCCACAGTGCCA(AGGCATTACACAGCATTTGA	720

Qy	1973	GGTCTTCACCCACTACGACCTCCTCACTCTCAATGGCTCCAAAGGTGCCTGAGGGGCACAA	20332
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Qy	2033	GGCCAGCTTGCTCTGGAGGACACAACCTGCCACACAGGACTGTCAGCGCGCTACCAGCATG	2092
Db	781	GGCCAGCTTGCTCTGGAGGACACAACCTGCCACACAGGACTGTCAGCGCGCGCTACCAGCATG	840
Qy	2093	TGCCAACCTTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACAT	2152
Db	841	TGCCAACCTTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACAT	900
Qy	2153	TGATTGCCAGTGGGTGGGATATCACAGATGTGGGCCCCGGGAATTATATCTTCACAGTGTAT	2212
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Qy	2213	TGTGAACCCCCTCATTAAGTGGCAGAGTCAGATTTCCTCAAACAATATGTCGCAGTGC CG	2272
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Qy	2333	AGCCAATGCAGAATCTCCCTGGAGCAGGACAGCGTCTCAGGAACAACCTCATCTGAAG	2392
Db	1081	AGCCAATGCAGAATCTCCCTGGAGCAGGACAGCGTCTCAGGAACAACCTCATCTGAAG	1140
Qy	2393	CTGTCACTGCACACTCCTAGCTGCTGCCGATACACCATACCTCACTGTTATTTGGAGCCA	2452
Db	1141	CTGTCACTGCACACTCCTAGCTGCTGCCGATACACCATACCTCACTGTTATTTGGAGCCA	1200
Qy	2453	TGCCCTTTCACAGAGTCCCAACTCAGAGGAAAAAGGCCAGTGCCCAAGGGGCACCAAGAACC	2512
Db	1201	TGCCCTTTCACAGAGTCCCAACTCAGAGGAAAAAGGCCAGTGCCCAAGGGGCACCAAGAACC	1260
Qy	2513	TGCTCAGGAAGCCTTTTGATGGCMAGATCACCAATCAGATGGTATTTGCTCCCTCAGGAT	2572
Db	1261	TGCTCAGGAAGCCTTTTGATGGCMAGATCACCAATCAGATGGTATTTGCTCCCTCAGGAT	1320
Qy	2573	GGCTCTGGGCTGCGCCCTAAGGCGCTGTGGCCTATGGAAATATGCTCTCAGGCTTTGCTC	2632
Db	1321	GGCTCTGGGCTGCGCCCTAAGGCGCTGTGGCCTATGGAAATATGCTCTCAGGCTTTGCTC	1380
Qy	2633	AGCTGAGCTCCTCTCTGTGAAGAAACCCAGTCTACCTCGAATCTTGCACACAGATTCOG	2692
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Qy	2693	GGATTACAGGAGCTCTCAGTTTTCTTAGGATGACACTATGGCCAGTCCCCATCTAAGTGG	2752
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Qy	2753	TGCTTTGCCAAATCTCTTGAGGAGATATAGCACAGAGGACCAAAAATACACAGCAGGTAGTG	2812
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Qy	2813	TTAGCTCTCTGTAGGAGCTCAAGCAACACAATTTGTATCAAAATACAACTCGGACAG	2872
Db	1561	TTAGCTCTCTGTAGGAGCTCAAGCAACACAATTTGTATCAAAATACAACTCGGACAG	1620
Qy	2873	AAGCTGCTGGATCCAACTCTTCTTCATCTGTGTTATTTAGMACTCACCTTCACACTC	2932
Db	1621	AAGCTGCTGGATCCAACTCTTCTTCATCTGTGTTATTTAGMACTCACCTTCACACTC	1680
Qy	2933	TGTTCTTTAGTGTCTTACCTTTATCTTACCACACACATGGGTGTTTCTATTATCTCTGG	2992
Db	1681	TGTTCTTTAGTGTCTTACCTTTATCTTACCACACACATGGGTGTTTCTATTATCTCTGG	1740
Qy	2993	AAGCACAGACTCTGGGCACTCCCTTTATTCGCTGATGGGCGCAACACCAACAGTTACGGAGT	3052
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Qy	3053	GCTTGAGAGGGGCAAGTTTCA	CAGAAATGCGCAGATAGGGCTTCTCTACAGACAGCAA	3112
Db	1801	GCTTGAGAGGGGCAAGTTTCA	CAGAAATGCGCAGATAGGGCTTCTCTACAGACAGCAA	1860
Qy	3113	GAGTAGGCCAAGCAGAAAGACTGCT	GAGGTAACTACCGACCCACGCCCTCTGTCAGGGCTC	3172
Db	1861	GAGTAGGCCAAGCAGAAAGACTGCT	GAGGTAACTACCGACCCACGCCCTCTGTCAGGGCTC	1920
Qy	3173	TGCCAAGGAAATTAATATGACCATTTAC	CTGCAGCGCAGTGTGCTCTCTCTACAGATCAC	3232
Db	1921	TGCCAAGGAAATTAATATGACCATTTAC	CTGCAGCGCAGTGTGCTCTCTCTACAGATCAC	1980
Qy	3233	CAGCATCTCAGGATTTGCTTAACTCTCAAGTCTCAAC	CCAGTGTCTGAAGTGAACCTTTG	3292
Db	1981	CAGCATCTCAGGATTTGCTTAACTCTCAAGTCTCAAC	CCAGTGTCTGAAGTGAACCTTTG	2040
Qy	3293	CATTGAATAAATTTTTGCCATGGAAGAAACATCAAA	CAAGCCACTCATCTCTACAGAGAT	3352
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Qy	3353	AAGAAAAAAGTTTGGCAGAGCAAGAGACAGAAAGAC	CCGTGGAGAAATCAGAAGGGGGAAC	3412
Db	2101	AAGAAAAAAGTTTGGCAGAGCAAGAGACAGAAAGAC	CCGTGGAGAAATCAGAAGGGGGAAC	2160
Qy	3413	AGTCAGTTTAGTTTAAAGATGGGAACCTGGG	AGAGGCCACCATTCCTGCTTGAATGGGGCTCT	3472
Db	2161	AGTCAGTTTAGTTTAAAGATGGGAACCTGGG	AGAGGCCACCATTCCTGCTTGAATGGGGCTCT	2220
Qy	3473	GATTTGCTCTTGCTCAAGTGGAAATAAAACCCCAT	TGGTCTTTTGACA	3519
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RESULT 9				
AX323481				
LOCUS	AX323481	2268 bp	DNA	linear
DEFINITION	Sequence 3 from Patent WO0192495.			
ACCESSION	AX323481			
VERSION	AX323481.1	GI:18094236		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1			
TITLE	Meyers, R.			
JOURNAL	A human lysyl oxidase (47765) and uses thereof			
FEATURES	Patent: WO 0192495-A 3 06-DEC-2001;			
source	Millennium Pharmaceuticals, Inc. (US)			
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ORIGIN	Query Match Best Local Similarity Matches 2265; Conservative	62.6%; 99.9%; 0;	Score 2263.2; Pred. No. 0; Mismatches 0;	DB 6; Length 2268; Indels 0; Gaps
QY	120	ATGGCGTGTGTCCTCCACAGCACCCTCTTTCTGTTCTGCTGCTGCTAGGCCAGCCCCCT	179	
Db	1	ATGGCGTGTGTCCTCCACAGCACCCTCTTTCTGTTCTGCTGCTGCTAGGCCAGCCCCCT	60	
QY	180	CCAGAGGCACAGTCACTGGGCACCACTAAGTCAGCTCCGCTGGTGCCAGAGCAAG	239	
Db	61	CCAGAGGCACAGTCACTGGGCACCACTAAGTCAGCTCCGCTGGTGCCAGAGCAAG	120	
QY	240	CCAGAGGGCGCCCTGGAGTGTCTGCAACAGGSCACTGGGGCACCGTGTGATCAAC	299	
Db	121	CCAGAGGGCGCCCTGGAGTGTCTGCAACAGGSCACTGGGGCACCGTGTGATGAC	180	
QY	300	AACATTGCTATCCAGAGGSCACAGTGGTCTGGCGCAGCTGGCTTCCAAGCTGCCTTG	359	
Db	181	AACATTGCTATCCAGAGGSCACAGTGGTCTGGCGCAGCTGGCTTCCAAGCTGCCTTG	240	
QY	360	ACCTGGGCCCACAGTGCAGTAGCCCAAGGGAGGGACCCATCTGGGTGACAAATGTG	419	
Db	241	ACCTGGGCCCACAGTGCAGTAGCCCAAGGGAGGGACCCATCTGGGTGACAAATGTG	300	
QY	420	CGCTGTGTGGGCACAGAGAGCTCCTTTGGACCACTGGCGGTCTTAATGGCTGGGGAGTCA	479	
Db	301	CGCTGTGTGGGCACAGAGAGCTCCTTTGGACCACTGGCGGTCTTAATGGCTGGGGAGTCA	360	
QY	480	GACTCGAGTCACTCAGNAGACGTAGGGGTGATATGCACCCCGGCCCATCTGGCTAC	539	
Db	361	GACTCGAGTCACTCAGNAGACGTAGGGGTGATATGCACCCCGGCCCATCTGGCTAC	420	
QY	540	CTTTCTGAATCTCTTCAAATGCCCTTTGGGCCCAAGGGCGCGGTGTGAGGAGTGGG	599	
Db	421	CTTTCTGAATCTCTTCAAATGCCCTTTGGGCCCAAGGGCGCGGTGTGAGGAGTGGG	480	
QY	600	CTCAAGCCCATCTTGCAGTGCACAAGCAGCATAGCCCACTAGCCAGGAGGCGCTGGAG	659	
Db	481	CTCAAGCCCATCTTGCAGTGCACAAGCAGCATAGCCCACTAGCCAGGAGGCGCTGGAG	540	
QY	660	GTCAAGTATGAGGGCCACTGGCGGAGGTGTGTGACAGAGGCTGGACCATGAACACAGC	719	
Db	541	GTGAAGTATGAGGGCCACTGGCGGAGGTGTGTGACAGAGGCTGGACCATGAACACAGC	600	
QY	720	AGSGTGTGTGGGATGTCTGGGCTTCCCGACGAGGTGCTGTGACAGCCACTACTAC	779	
Db	601	AGSGTGTGTGGGATGTCTGGGCTTCCCGACGAGGTGCTGTGACAGCCACTACTAC	660	
QY	780	AGGAAGTCTGGGATCTGAAGATGAGGAGCCCTTAAGTCTAGGCTGAAGAGCCTGACGAAT	839	
Db	661	AGGAAGTCTGGGATCTGAAGATGAGGAGCCCTTAAGTCTAGGCTGAAGAGCCTGACGAAT	720	
QY	840	AAGAACTCTTCTGGATCCACAGGTCACTGGCTGGGACAGAGCCACATGGCCAAC	899	
Db	721	AAGAACTCTTCTGGATCCACAGGTCACTGGCTGGGACAGAGCCACATGGCCAAC	780	
QY	900	TGCCAGGTGCAAGTGGCTCCAGGCCCGGGCAAGCTCGGCCAGCCTGCCCGAGTGGCATG	959	
Db	781	TGCCAGGTGCAAGTGGCTCCAGGCCCGGGCAAGCTCGGCCAGCCTGCCCGAGTGGCATG	840	
QY	960	CATGCTGTGCTAGCTGTGTGGCAGGGCCCTCACTTCGGCCACCGGAACAAGCCACAA	1019	
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QY	1020	CGCAAGGGTCTTGGCAGAGGAGCCGAGGGTGGCTCGGCTCCGGGGCCAGGTGGGC	1079	
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QY	1080	GAGGGCGGGTGAAGTGTCTATCAACCGCCAGTGGGGCACGGTCTGTGACCAAGTGG	1139	
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QY	2220	CCCCACTATGAAGTGGCAGAGTCAGATTCTCCAACAATATGCTGCAGTGCGGTCCAAG	2279
Df	2101	CCCCACTATGAAGTGGCAGAGTCAGATTCTCCAACAATATGCTGCAGTGCGGTCCAAG	2160
QY	2280	TATGATGGCACACGGGTCTCGCTGCCAACATGCACACAGGGAATTCATACCAGCCAAT	2339
Df	2161	TATGATGGCACACGGGTCTCGCTGCCAACATGCACACAGGGAATTCATACCAGCCAAT	2220
QY	2340	GCAAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATC	2387
Df	2221	GCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATC	2268
RESULT 10	AF395336	2271 bp mRNA linear PRI 05-NOV-2001	
LOCUS	Homo sapiens lysyl oxidase-like 4 (LOXL4)	mRNA, complete cds.	
DEFINITION	Homo sapiens lysyl oxidase-like 4 (LOXL4)		
ACCESSION	AF395336		
VERSION	AF395336.1	GI:16660130	
KEYWORDS	.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
REFERENCE	1 (bases 1 to 2271)		
AUTHORS	Asuncion,L.P., Fogelgren,B., Fong,K.S.F.T., Kim,Y. and Csizsar,K.		
TITLE	A novel human lysyl oxidase-like gene (LOXL4) on chromosome 10q24 has an altered SRCR domain and is down-regulated by H-ras		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2271)		
AUTHORS	Asuncion,L.P., Fogelgren,B., Fong,K.S.F.T., Kim,Y. and Csizsar,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-JUN-2001) Pacific Biomedical Research Center,		
FEATURES	University of Hawaii, 1993 East West Road, Honolulu, HI 96822, USA Location/Qualifiers		
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ORIGIN			
Query Match		62.5%	Score 2258.2; DB 9; Length 2271;
Best Local Similarity		99.6%; Pred. No. 0;	
Matches 2263; Conservative		0; Mismatches	8; Indels 0; Gaps 0;
QY	120	ATGCGTGGTCCCCACAGCACCGCTCTTCTGTCTGCTGCTGCTAGGCACGCCCT	179

Db	1	ATGGCGTGGTCCCCACACAGCCACCTCTTTCTGTCTCTGTCTGTCTGTAGCCACAGCCCCCT	60
Qy	180	CCAGCAGGCCACACAGTCACTGGGCACCACTAAGCTTCGGCTGGTGGGCACAGAGCAAG	239
Db	61	CCAGCAGGCCACACAGTCACTGGGCACCACTAAGCTTCGGCTGGTGGGCACAGAGCAAG	120
Qy	240	CCAGAGAGGGCCGCTTGAGAGTGTGCACAGGCCACAGTGGGGACACCGTGTGTGATGAC	299
Db	121	CCAGAGAGGGCCGCTTGAGAGTGTGCACAGGCCACAGTGGGGACACCGTGTGTGATGAC	180
Qy	300	AACCTTGTCTATCCAGSAGGCCACAGTGGCTTTCGCCACAGCTGGGGCTTCGAAGCTGCCTTG	359
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Qy	360	ACCTGGGCCACAGTGGCAAGTACGGCCAAAGGGAGGGACCCATCTCGCTGGACAAATGTG	419
Db	241	ACCTGGGCCACAGTGGCAAGTACGGCCAAAGGGAGGGACCCATCTCGCTGGACAAATGTG	300
Qy	420	CGCTGTGTGGGCACAGAGAGTCTCTTGGACCAAGTCGCGGTCTAATGCTGGGGAGTCAGT	479
Db	301	CGCTGTGTGGGCACAGAGAGTCTCTTGGACCAAGTCGCGGTCTAATGCTGGGGAGTCAGT	360
Qy	480	GACTGCAGTCACTCAGAAGACGTAGGGTGATATGCCACCCCCCGCGGCCCATCTGGTGCATC	539
Db	361	GACTGCAGTCACTCAGAAGACGTAGGGTGATATGCCACCCCCCGCGGCCCATCTGGTGCATC	420
Qy	540	CTTTCTGAAACTGTCTCCAAATGSCCTTCGGGCCACAGGGCCGGCGCTTGGAGAGGTCCGG	599
Db	421	CTTTCTGAAACTGTCTCCAAATGSCCTTCGGGCCACAGGGCCGGCGCTTGGAGAGGTCCGG	480
Qy	600	CTCAAGCCCATCTCTTGGCAGTGCCAAGCAGCATAGCCAGTCAGCCGAGGGAGCCGTGGAG	659
Db	481	CTCAAGCCCATCTCTTGGCAGTGCCAAGCAGCATAGCCAGTCAGCGAGGGAGCCGTGGAG	540
Qy	660	GTGAAGTATGAGGGCCACTTGGCGGACAGTGTGTGACACAGGCTGGACATGAACAAACAGC	719
Db	541	GTGAAGTATGAGGGCCACTTGGCGGACAGTGTGTGACACAGGCTGGACATGAACAAACAGC	600
Qy	720	AGGTCGTGTGGGATGCTGGGCTTCCCGACGAGGTGCCTGTGACACCCACTACTATC	779
Db	601	AGGTCGTGTGGGATGCTGGGCTTCCCGACGAGGTGCCTGTGACACCCACTACTATC	660
Qy	780	AGGAAAGTCTGGATCTGAAGATGAGGACCCCTAAGTCTAGGCTGAAGAGCCTCAGCAAT	839
Db	661	AGGAAAGTCTGGATCTGAAGATGAGGACCCCTAAGTCTAGGCTGAAGAGCCTCAGCAAT	720
Qy	840	AAGAACTCTTCTGGAATCCACAGTCACTTGCCTGGGGAACAGAGCCCCCATCGCCAAAC	899
Db	721	AAGAACTCTTCTGGAATCCACAGTCACTTGCCTGGGGAACAGAGCCCCCATCGCCAAAC	780
Qy	900	TGCCAGGTGCAGTGGCTCCAGCCGGGGCAAGCTGGCGCCAGCTGCCAGGTGGCATG	959
Db	781	TGCCAGGTGCAGTGGCTCCAGCCGGGGCAAGCTGGCGCCAGCTGCCAGGTGGCATG	840
Qy	960	CATGCTGTGCTCAGTGTGTGACAGGGCTCACTTCCGCCCCACGAAAGCAAAAGCCACAA	1019
Db	841	CAGCTGTGCTCAGTGTGTGACAGGGCTCACTTCCGCCCCACGAAAGCAAAAGCCACAA	900
Qy	1020	CGCAAAAGGTCCTGGGCACAGAGGCCGAGGGTGGCTCTGGCTCCGGGGCCACAGGTGGCC	1079
Db	901	CGCAAAAGGTCCTGGGCACAGAGGCCGAGGGTGGCTCTGGCTCCGGGGCCACAGGTGGCC	960
Qy	1080	GAGGGCCGGGTGGAGTGTCTATGAACCGCCAGTGGGGCAAGTCTGTGTGACCAACAGTGG	1139
Db	961	GAGGGCCGGGTGGAGTGTCTATGAACCGCCAGTGGGGCAAGTCTGTGTGACCAACAGTGG	1020
Qy	1140	AACCTCATCTCTGCCAGTGTGCTGTGCTCAGCTGGGCTTTTGCTCTGTCTCGGAGGCC	1199
Db	1021	AACCTCATCTCTGCCAGTGTGCTGTGCTCAGCTGGGCTTTTGCTCTGTCTCGGAGGCC	1080
Qy	1200	CTCTTTGGGGCCCGGTGGGCCCAAGGGCTAGGGGCCCATTCACCTGAGTGAGGTGCCTGC	1259

QY 1711 GTGCACAGACCTGGTGTATGAAGCCGAGCTAGTGTGAGGAGACGGCCCTACTTGGAGGACC 1770
Db 121 GTGCACAGACCTGGTGTATGAAGCCGAGCTAGTGTGAGGAGACGGCCCTACTTGGAGGACC 180
QY 1771 GCCCGCTCAGCCAGCTGATTGTGSCCAGGAGAGAACTCCCTCTCCAAGTCTGCGGATC 1830
Db 181 GCCCGCTCAGCCAGCTGATTGTGSCCAGGAGAGAACTCCCTCTCCAAGTCTGCGGATC 240
QY 1831 ACATGGACTGGCCCTACGGATACCGCCGCTATTGGCCCTTCTCCACACAGATCTACAATC 1890
Db 241 ACATGGACTGGCCCTACGGATACCGCCGCTATTGGCCCTTCTCCACACAGATCTACAATC 300
QY 1891 TGGCCCGACTGACTTTCGTCGCAAGAGCTGACCGGATAGCTGGTTTGGCAGAGTGC 1950
Db 301 TGGCCCGACTGACTTTCGTCGCAAGAGCTGACCGGATAGCTGGTTTGGCAGAGTGC 360
QY 1951 ACAGGCATTACACAGCATTTAGAGTCTTACCCCACTACGACCTCCCTCAATGGCT 2010
Db 361 ACAGGCATTACACAGCATTTAGAGTCTTACCCCACTACGACCTCCCTCAATGGCT 420
QY 2011 CCAAGTGGCTGAGGGGACAAAGCCAGCTTCTGTGTGGAGGACACAACTGCCCCACAG 2070
Db 421 CCAAGTGGCTGAGGGGACAAAGCCAGCTTCTGTGTGGAGGACACAACTGCCCCACAG 480
QY 2071 GACTGCAGCGCGCTACGATGTGCCAACTTTTGAGAACAGGAGTGACTGTAGGCTGT 2130
Db 481 GACTGCAGCGCGCTACGATGTGCCAACTTTTGAGAACAGGAGTGACTGTAGGCTGT 540
QY 2131 GGGACACTACCGGCATGACATTTGACAGTGGGTGGATATCACAGATGTGGGCCCG 2190
Db 541 GGGACACTACCGGCATGACATTTGACAGTGGGTGGATATCACAGATGTGGGCCCG 600
QY 2191 GGAATTATATCTCCAGTGATTTGTAACCCCACTATGAAGTGGCAGAGTCAGATTTCT 2250
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QY 2251 CCAACAATATGCTCAGTGGCGCTGCAAGTATGATGGGACCCGGTCTGCTGCACAACT 2310
Db 661 CCAACAATATGCTCAGTGGCGCTGCAAGTATGATGGGACCCGGTCTGCTGCACAACT 720
QY 2311 GCCACACAGGGAATTCATACCCAGCAATGCAGAACTCTCCCTGGACAGCAAGCGTC 2370
Db 721 GCCACACAGGGAATTCATACCCAGCAATGCAGAACTCTCCCTGGACAGCAAGCGTC 780
QY 2371 TCAGGAACAACCTCATCTGAAGCTGTCACTGCACACTCTAGTGTGCGGATACACCCAG 2430
Db 781 TCAGGAACAACCTCATCTGAAGCTGTCACTGCACACTCTAGTGTGCGGATACACCCAG 840
QY 2431 ATACCTCAGCTTATTGGAGCCATGCCCTTACAGAGTCCCAACTCAGAGGAAAGGGCCA 2490
Db 841 ATACCTCAGCTTATTGGAGCCATGCCCTTACAGAGTCCCAACTCAGAGGAAAGGGCCA 900
QY 2491 GTGCCAAGGGGACCAAGAACTGCTCAGAGAGCTTTTATGAGCAAGATCACAATCCA 2550
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Db 1141 GCCCAGTCCCCCATCTAAGTGGTCTTTGCAAAATGCTCTGGAGAGTATAGGACAGGGA 1200

QY 2791 CCAAAATACACAGAGCTAGTGTAGTCTCTGTAGAGCTCAAAAGCAACACAACTTGT 2850
Db 1201 CCAAAATACACAGAGCTAGTGTAGTCTCTGTAGAGCTCAAAAGCAACAACTTGT 1260
QY 2851 ATCAAAATCACAACCTGGCAGAGAACTGGTGGATCCAATCCCTTTCTTATCTGTGTTAT 2910
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QY 3091 GGGCCCTTCTTACAGAGCAGCAAGAGTAGGCCAAGCAGAGAACTGCTGAGGTAACACCGA 3150
Db 1501 GGGCCCTTCTTACAGAGCAGCAAGAGTAGGCCAAGCAGAGAACTGCTGAGGTAACACCGA 1560
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QY 3211 GTCTGCTCTCTCAGGATCACCGCATCTCAGATTTGCTTAACCTCAAGTCTCAAC 3270
Db 1621 GTCTGCTCTCTCAGGATCACCGCATCTCAGATTTGCTTAACCTCAAGTCTCAAC 1680
QY 3271 CAAGTGTCTGAAGTGAACCTTTTGCATTGAATAAATTTTGCATGGAAGAAATCAAAACA 3330
Db 1681 CAAGTGTCTGAAGTGAACCTTTTGCATTGAATAAATTTTGCATGGAAGAAATCAAAACA 1740
QY 3331 AGCCACTCATCTCTCAGAGATAAGAAACAAAGTTTGGCAGAGCAAGACAGACCG 3390
Db 1741 AGCCACTCATCTCTCAGAGATAAGAAACAAAGTTTGGCAGAGCAAGACAGACCG 1800
QY 3391 TGGAGAAATCAGAAGGGGAAACAGTCAGTTTATGTTTANGATGGAACCTGGGAAGGCCAC 3450
Db 1801 TGGAGAAATCAGAAGGGGAAACAGTCAGTTTATGTTTANGATGGAACCTGGGAAGGCCAC 1860
QY 3451 CATCTCTGCTTGTATGGGCTCTGATTTGCTCTTGTCTCAAGTGAATATAACCCCATGTC 3510
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QY 3511 TTCTTGACATGATTTGATCTTTTCTCCACTGAGACACACTTAAGTATGATCTTACA 3570
Db 1921 TTCTTGACATGATTTGATCTTTTCTCCACTGAGACACACTTAAGTATGATCTTACA 1980
QY 3571 GGACTGACACCTTAATGCCAATAAAGTTGCTCATTTGGACTGCT 3616
Db 1981 GGACTGACACCTTAATGCCAATAAAGTTGCTCATTTGGACTGCT 2026

RESULT 12
AF338440

LOCUS AF338440 2274 bp mRNA linear ROD 11-JUL-2001
DEFINITION Mus musculus lysyl oxidase-related protein C (LoxC) mRNA, complete cds.

ACCESSION AF338440
VERSION AF338440.1 GI:14669468

KEYWORDS
SOURCE Mus musculus.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2274)
REFERENCE
AUTHORS Ito,H., Akiyama,H., Iguchi,H., Iyama,K., Miyamoto,M., Ohsawa,K. and
Nakamura,T.
TITLE Molecular cloning and biological activity of a novel lysyl


```
Db 1501 ACAGAAATGCCCTTGACAGAGTGTACAGAGCATGGCGCGGTGCACCTGTTCCCAAGGCCCA 1560
QY 1677 GGGCGCTTCTCGCTGGAGTCTCTCTGATGACAGTGCACACAGCTGGTGTATGAACGCC 1736
Db 1561 GGGCGCTTCTCGCTGGCGTGTCTGTATGAACAGTGTCTCAGACCTCGTGTATGAACGCC 1620
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QY 2037 AGCTTCTGTCTGGAGGACACAACTGCCACAGGACTGCAGCGGCGCTACGATGTGCC 2096
Db 1921 AGCTTCTGTCTAGAGATACAACTGCCCTCAGGAGTGCAGCGGCGCTATGATGTGCC 1980
QY 2097 AACTTTGGAGAACAGGAGTGAAGTGTAGGCTGTGGGACACCTACCGGCATGATGAT 2156
Db 1981 AACTTTGGGAAACAGGAGTGGTGTAGGCTGTGGGACACCTACCGGCATGATGAT 2040
QY 2157 TGCAGTGGGTGATATCAGATGTGGGCGCGCGGAAATATATCTTCCAGGTGATGTG 2216
Db 2041 TGCAGTGGGTGATATCAGATGTGGGCGCGCGGAAATATATCTTCCAGGTGATGTG 2100
QY 2217 AACCCCACTATGAAGTGGCAGAGTCAAGATTTCTTCCAAATATGTGTCAGTGCCTGTC 2276
Db 2101 AACCCCAAAACGATGTGAGAGTCCGATTTCTTCCAAATATGATAGTGCCTGTC 2160
QY 2277 AAGTATGATGGCACCGGCTGTGCTGCACAACTGCCACAGGAAATTCATACCCAGCC 2336
Db 2161 AAGTATGATGACAGCAGTGTGTTGCACTGCCACAGGAGATTCCTACCGAGCC 2220
QY 2337 AATGCAAACTTCTCCCTGGAGGAGGACAGGCTCTCAGGAAACACCTCATCTGA 2390
Db 2221 AATGCAAGCTTCTCCCTGGAGGAGGACAGGCTCTCAGGAAACACCTCATCTGA 2274

RESULT 13
AL139241/c
LOCUS
DEFINITION Human DNA sequence from clone RP11-34A14 on chromosome 10, complete
sequence.
ACCESSION AL139241
VERSION AL139241.11 GI:16508186
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188192)
Direct Submission
Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Oct 29, 2001 this sequence version replaced gi:14575095.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
```

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPep; information on the WormPep database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep

This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>

RP11-34A14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-34A14. The true left end of clone RP11-439D8 is at 146755 in this sequence. The true right end of clone RP11-594J24 is at 52695 in this sequence.

Location/Qualifiers

1..188192

organism="Homo sapiens"

db_xref="taxon:9606"

/chromosome="10"

/clone="RP11-34A14"

/clone.lib="RPCI-11.1"

20413..20507

note="Sequence from overlapping clone RP11-594J24 (AL355301). Assembly confirmed by restriction digest."

101262..101305

note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."

BASE COUNT 49922 a 40190 c 42007 g 56073 t

ORIGIN

Query Match 36.1%; Score 1303.8; DB 9; Length 188192;

Best Local Similarity 99.8%; Pred. No. 8.3e-296;

Matches 1305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 TGCCACACAGGGAATTCATACCCAGCCCAATGCAGAACTTCCCTGGAGCAGGAACAGCGT 2369

Db 81880 TGGCCACACAGGGAATTCATACCCAGCCCAATGCAGAACTTCCCTGGAGCAGGAACAGCGT 81821

QY 2370 CTCAGGAACAACCTCATCTGAAGCTGTCACTGCACACTCTCTAGCTGCTGCCATACCA 2429

Db 81820 CTCAGGAACAACCTCATCTGAAGCTGTCACTGCACACTCTCTAGCTGCTGCCATACCA 81761

QY 2430 GATACCTCAGCTTATTTGGAGCCATGCCCTTTCACAGAGTCCCAACTCAGAGGAAAGGGCC 2489

Db 81760 GATACCTCAGCTTATTTGGAGCCATGCCCTTTCACAGAGTCCCAACTCAGAGGAAAGGGCC 81701

QY 2490 AGTGCCAAAGGGGACCAAGAACCTGCTCAGGAAGCCTTTTGATGGCAAGATCACCAATCC 2549

Db 81700 AGTGCCAAAGGGGACCAAGAACCTGCTCAGGAAGCCTTTTGATGGCAAGATCACCAATCC 81641

QY 2550 AGATGGTATTGCTCCCTCAGGATGGCTCTGGGCTGCGCCCTGAAGGGCTGTGGCTATGG 2609

Db 81640 AGATGGTATTGCTCCCTCAGGATGGCTCTGGGCTGCGCCCTGAAGGGCTGTGGCTATGG 81581

QY 2610 AATATGCTCTCCAGGCTTTGCTCAGCTGAGTCTCTTCTGTAAGGAACCCAGTCATCC 2669

Db 81580 AATATGCTCTCCAGGCTTTGCTCAGCTGAGTCTCTTCTGTAAGGAACCCAGTCATCC 81521

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QY 2670 CTGAATCTTGGCCACAGAGATCCGGGATTCAGGAGCTCTCAGTTTCTTAGGGATGCACTAT 2729
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QY 2730 GGCCCAAGTCCCCCATCTAAGTGGTGGCTTTGCAAAATCTCTTGGAGGAGTAGTAGCAGAGG 2789
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Db 81460 GGCCCAAGTCCCCCATCTAAGTGGTGGCTTTGCAAAATCTCTTGGAGGAGTAGTAGCAGAGG 81401
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QY 2790 ACCAAAATACAGAGAGTAGTGTAGTCTCTGCTAGAGCTCAAGCAACACACTTTG 2849
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Db 81400 ACCAAAATACAGAGAGTAGTGTAGTCTCTGCTAGAGCTCAAGCAACACACTTTG 81341
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QY 2850 TATCAAAATACAACTGGCAGAGAGCTGGTGATCCAAATCTCTTTCTTCTATCTGTGTTA 2909
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Db 81340 TATCAAAATACAACTGGCAGAGAGCTGGTGATCCAAATCTCTTTCTTCTATCTGTGTTA 81281
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QY 3030 GCCAACACCAACAGTTACGGAGTCTTGAAGGGGCAAGTTTTCAGAGAAATGGCCAGAT 3089
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QY 3090 AGGGCTTCTCTACAGAGCAGCAAGATAGCCCAAGCAGAGAAAGCTCTCGAGTAAACAGG 3149
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Db 81040 ACCCCAGCCCTCTCAGGGCTCTGCAAGGAATATATGACCACTTACCTGGCAGGC 80981
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QY 3210 AGTCTGCTCTCTCAGGATCACAGCATCTCAGATTGCTTAACTTCAAGTCTCAA 3269
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Db 80980 AGTCTGCTCTCTCAGGATCACAGCATCTCAGATTGCTTAACTTCAAGTCTCAA 80921
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QY 3270 CCAAGTCTGGAAGTGAACCTTTCATTGTAATAATTTTGCCTGGAAGCAACATCAAAAC 3329
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QY 3330 AAGCCATCATCTCTACAGAGTAAGAAACAAGTTTGGCAGAGCAGAGACAGAGACC 3389
|||||
Db 80860 AAGCCATCATCTCTACAGAGTAAGAAACAAGTTTGGCAGAGCAGAGACAGAGACC 80801
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QY 3390 GTGGAGAAATCAGAAGGGGAAACAGTCAGTTTGTAGTAAAGATGGAACCTGGGAAAGGCCA 3449
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Db 80800 GTGGAGAAATCAGAAGGGGAAACAGTCAGTTTGTAGTAAAGATGGAACCTGGGAAAGGCCA 80741
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QY 3450 CCATTCTGCTGATGGGCTCTGATTGCTCTGCTCAGTGAATATAAACCCTATGCT 3509
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QY 3510 CTCTTTCATCATGATCTTGTATCTTTCTCCACTGAGACACACTTAAGTGTATGATCTTAC 3569
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Db 80680 CTCTTTCATCATGATCTTGTATCTTTCTCCACTGAGACACACTTAAGTGTATGATCTTAC 80621
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QY 3570 AGGACTGACACCTTAATGCCAATAAAGTTGCTCATTTATGACTGCT 3616
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Db 80620 AGGACTGACACCTTAATGCCAATAAAGTTGCTCATTTATGACTGCT 80574
|||||

RESULT 14
AC123374/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-275L16, *** SEQUENCING IN PROGRESS
***, 95 unordered pieces.
ACCESSION AC123374
VERSION AC123374.2 GI:21902551
KEYWORDS HTG; HTGS_PHASE1.

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SOURCE
ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 182222)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrooks, S.L., Amaratunge, H.C., Are, C.R., Ayele, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blenkenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, T., Brown, M., Bryant, N.P.,
Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dethorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., For, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, J., Garza, N., Gill, R.,
Gorell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Followay, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulyk, J., Hume, J., Jackson, L.E.,
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Karlssohn, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
Lorado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwionu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
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Rives, M., Rojas, A., Rojebokan, J., Rolie, M., Ruiz, S., Savary, G.,
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Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
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Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villa, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorri-la, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

TITLE

Direct Submission

Unpublished

REFERENCE
JOURNAL

2 (bases 1 to 182222)

Worley, K.C.

Direct Submission

Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 182222)

Worley, K.C.

Direct Submission

Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 18, 2002 this sequence version replaced gi:21240277.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GWLE
Center Clone name: CH230-275L16
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 1.990329

Consensus quality: 117047 bases at least Q40
Consensus quality: 124820 bases at least Q30
Consensus quality: 129800 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hqsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 95 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

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* 1162: contig of unknown length
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* 2308: gap of unknown length
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* 3792: contig of 1484 bp in length
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* 4996: contig of 1104 bp in length
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* 6197: contig of 1101 bp in length
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* 6297: gap of unknown length
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Query Match 34.2%; Score 1235.8; DB 2; Length 182222;
Best Local Similarity 81.8%; Pred. No. 8.4e-280;
Matches 1246; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

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 VERSION BC000594.1
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3422)
 Strausberg, R.
 Direct Submission
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/BTP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, F.J.,
 Tongson, E.E., Touchman, J.W., Tsurgenc, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 5 Row: a Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4505010.

FEATURES

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CDS

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Best Local Similarity 63.8%; Pred. No. 6.1e-190;

Matches 1400; Conservative	0; Mismatches 742; Indels 51; Gaps 5;
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Wed Apr 2 09:13:55 2003

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Search completed: April 1, 2003, 07:03:51
Job time : 19875 secs